Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for providing information about biological molecules, comprising the acts of:

~~receiving a user selection comprising one or more probe set identifiers that identify one or more probe-sets each comprising one or more probes disposed on one or more probe arrays and one or more intensity values detected from the probes of each probe-set, wherein the user performs the selection using a client side interface that is received over an internet network by a host side;~~

inputting one or more probe set identifiers that identify probes on an array, and a probe intensity value for each probe via a client side interface that is received over an internet network by a host side;

determining one or more alternative splice variants by iteratively fitting the probe set identifiers and the intensity values to a plurality of models of known genomic structure, such as exon structure or location data, protein family classification data, splice variant data, and genomic sequence data, associated with the alternative splice variants, wherein the fit of one or more of the models to the intensity values indicates the presence of the alternative splice variants and at least one of the probe arrays or at least one of the probe sets detects nucleic acids;

correlating at least one alternative splice variant with at least one annotation datum; and

providing to the user, over the internet network, a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

2. (Previously Presented) The method of claim 1, wherein:

one or more of the probe arrays is capable of diagnosing a disease or medical condition.

3. (Currently Amended) A method, comprising the acts of:

determining one or more alternative splice variants by iteratively fitting one or more user selected probe set identifiers that identify one or more probe sets disposed on one or more probe arrays and one or more intensity values detected from individual probes of the one or more probe-sets disposed on one or more probe arrays to a plurality of models of known genomic structure associated with the alternative splice variants, such as exon structure or location data, protein family classification data, splice variants data, and genomic sequence data, wherein a user selects the intensity values and one or more probe set identifiers that identify the probe-sets, and the fit of one or more of the models to the probe set identifiers and the intensity values indicates the presence of the alternative splice variants;

correlating at least one alternative splice variant with at least one annotation datum; and

providing to a user over an internet network a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

4. (Previously Presented) The method of claim 3, further comprising the act of:

receiving the user selection of the one or more probe set identifiers.

5. (Previously Presented) The method of claim 4, wherein:

the act of receiving includes the acts of the user originating the selection from a user computer, transmission of the selection over the internet network, and receipt of the selection at an Internet server.

6. (Cancelled)

7. (Previously Presented) The method of claim 3, wherein:

the one or more probe arrays comprise probes disposed on or in a support comprising beads, resins, gels, or microspheres.

8.-10. (Cancelled)

11. (Original) The method of claim 3, wherein:

the act of correlating includes correlating the at least one alternative splice variant with a gene and correlating the gene with the at least one annotation datum.

12. (Original) The method of claim 3, wherein:

the act of correlating includes correlating the at least one alternative splice variant with at least one other alternative splice variant of their common gene and correlating the at least one other alternative splice variant with the at least one annotation datum.

13. (Previously Presented) The method of claim 3, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum enables semantic zooming wherein magnification is determined on a user zoom selection.

14. (Original) The method of claim 13, wherein:

the annotation datum includes sequence information displayed on a sequence axis, and the semantic zooming is along a single dimension corresponding to the sequence axis.

15. (Previously Presented) The method of claim 3, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum is organized into a plurality of adjustable tiers that are represented so as to be capable of being collapsed, moved, or hidden in response to user tier selection.

16. (Previously Presented) The method of claim 3, wherein:

the graphical representation of the at least one annotation datum is represented in response to a user selection of an mRNA.

17. (Previously Presented) The method of claim 3, wherein:

the at least one annotation datum includes mRNA.

18. (Previously Presented) The method of claim 3, wherein:

the act of providing the graphical representation includes a representation of an alignment of a first alternative splice variant with a second alternative splice variant, wherein the first and second alternative splice variants are variants of a same gene.

19. (Previously Presented) The method of claim 18, wherein:

the alignment of the first and second alternative splice variants comprises a comparison of the first and second alternative splice variants to genomic sequence or sequence of the same gene.

20. (Previously Presented) The method of claim 3, wherein:

the act of providing the graphical representation includes graphically associating the alternative splice variant and the annotation datum.

21. (Previously Presented) The method of claim 3, wherein:

the act of providing the graphical representation includes representing a plurality of annotation data in a plurality of panes of a single graphical user interface.

22.-23. (Cancelled)

24. (Original) The method of claim 3, wherein:

the probe sets comprise probes constructed and arranged to detect mRNA expression.

25. (Previously Presented) The method of claim 24, wherein:

the probes comprise exon probes or junction probes.

26.-27 (Cancelled)

28. (Currently Amended) A system comprising:

an alternative splice variant evaluator that determines one or more alternative splice variants by iteratively fitting one or more user selected probe set identifiers that identify one or more probe sets disposed on one or more probe arrays and one or more intensity values detected from the probes of one or more probe-sets disposed on one or more probes arrays to a plurality of models of known genomic structure associated with the alternative splice variants, such as exon structure or location data, protein family classification data, splice variants data, and genomic sequence data, wherein a user selects the intensity values and one or more probe set identifiers that identify the probe-sets, and the fit of one or more of the models to the intensity values indicates the presence of the alternative splice variants;

an alternative splice variant data storage and annotation data correlator that correlates at least one alternative splice variant with at least one annotation datum; and

a user-service manager that provides to a user over an internet network a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

29. (Previously Presented) The system of claim 28, further comprising:

an input manager that receives the user a selection of the one or more probe set identifiers.

30. (Previously Presented) The system of claim 29, wherein:

the input manager receives the user selection over the Internet network .

31. (Previously Presented) The system of claim 28, wherein:

the probe sets include probes of a probe array nucleic acids.

32. (Previously Presented) The system of claim 28, wherein:

the graphical representation of the at least one alternative splice variant or of the at least one annotation datum enables semantic zooming wherein magnification is determined on a user zoom selection.

33. (Previously Presented) The system of claim 28, wherein:

the representation of the at least one annotation datum is represented in response to a user selection of an mRNA.

34. (Previously Presented) The system of claim 28, wherein:

the at least one annotation datum includes mRNA.

35. (Previously Presented) The system of claim 28, wherein:

the graphical representation includes a representation of an alignment of a first alternative splice variant with a second alternative splice variant, wherein the first and second alternative splice variants are variants of a same gene.

36. (Previously Presented) The system of claim 35, wherein:

the alignment of the first and second alternative splice variants comprises a comparison of the first and second alternative splice variants to genomic sequence or sequence of the same gene.

37. (Previously Presented) The system of claim 28, wherein:

the graphical representation includes graphically associating the alternative splice variant and the annotation datum.

38.-39. (Cancelled)

40. (Original) The system of claim 28, wherein:

the probe sets comprise probes constructed and arranged to detect mRNA expression.

41. (Previously Presented) The system of claim 40, wherein:

the probes comprise exon probes or junction probes.

42. (Cancelled)

43. (Currently Amended) A genomic web portal, comprising:

an input manager that receives a user selection comprising one or more probe set identifiers that identify one or more probe-sets each comprising one or more probes disposed on one or more probe arrays and one or more intensity values detected from ~~the~~ individual probes of each probe-set, wherein the user performs the selection using a client side interface that is received over an internet network by a host side;

an alternative splice variant evaluator that determines one or more alternative splice variants by iteratively fitting the probe set identifiers and intensity values to a plurality of models of known genomic structure associated with the alternative splice variants, such as exon structure or location data, protein family classification data, splice variants data, and genomic sequence data, wherein the fit of one or more of the models to the probe set identifiers and the intensity values indicates the presence of the alternative splice variants;

an alternative splice variant data storage and annotation data correlator that correlates at least one alternative splice variant with at least one annotation datum; and

an output manager that provides to the user over the Internet network a graphical representation of the at least one alternative splice variant and the correlated annotation datum.

44. (Previously Presented) The genomic web portal of claim 43, wherein:

the graphical representation of the at least one annotation datum comprises a user selection of an mRNA.

45. (Previously Presented) The genomic web portal of claim 43, wherein:

the at least one annotation datum includes mRNA.